

Abstract

ABSTRACT

BACKGROUND

Polymicrobial etiology of periodontal disease and importance of dental plaque in its initiation and progression have been extensively documented. Transition from periodontal health to disease is associated with shift in the structure of bacterial community that inhabits subgingival niche. Technological advancements in DNA sequencing and newer bioinformatics tools have enabled understanding the complexity of subgingival microbiome in periodontal health and disease.

Though pocket associated biofilm has been extensively researched, chronic periodontitis characterized by gingival recession with gingival inflammation is less often studied in terms of its microbial community. The aim of this study is to identify and characterize subgingival microbiome using Next Generation Sequencing (NGS) Technology in periodontal health and gingival recession.

MATERIALS AND METHODS

A total of eight subgingival plaque samples, comprising four samples from periodontally healthy sites and four from sites with gingival recession were collected and analyzed. The subgingival microbiome was investigated with NGS technology using Illumina sequencing method. Amplicons from V3-V4 hypervariable regions of 16S rRNA gene were sequenced. Results obtained were represented according to taxonomic classification system of

bacteria, and individual comparisons were depicted through tables, graphs and phylogenetic tree.

RESULTS

Among healthy sites, a total of 27 phyla, 558 genera and 1063 species were identified and among gingival recession sites 29 phyla, 641 genera and 1279 were identified. No significant differences were found at phylum and genus level between health and disease sites although disease-associated microbes were found in greater abundance in gingival recession sites than healthy sites and health-associated microbes were identified in lower abundance in disease. At species level a distinct microbiome was observed for both groups, with 161 species uniquely present in healthy sites and 381 species uniquely present in gingival recession sites.

CONCLUSION

The diverse microbial composition observed in periodontal health and disease represents a distinct dysbiotic process. Understanding the differences in composition of subgingival microbial community provides a broader insight into the pathogenesis of periodontitis.

KEYWORDS

Subgingival Microbiome, Illumina Sequencing, Next Generation Sequencing, 16S rRNA, Gingival Recession, Chronic Periodontitis, Periodontal Pocket, Dysbiosis.